AMENDMENTS TO THE CLAIMS

This listing of the claims replaces all prior listings and versions:

1-122. (canceled)

- 123. (currently amended): A method for preparing a library of regulatory DNA sequences from a cell, the method comprising:
 - (a) providing a cell nucleus, wherein the nucleus comprises cellular chromatin;
- (b) contacting the nucleus with a first enzyme, wherein the first enzyme reacts with accessible regions of cellular chromatin;
 - (c) deproteinizing the cellular chromatin to generate deproteinized DNA;
- (d) contacting the deproteinized DNA with a second enzyme to generate <u>a</u> <u>plurality of different DNA fragments</u>;
- (e) contacting the DNA fragments obtained in step (d) with a population of vector molecules, wherein the vector molecules comprise a first end that is compatible with the first enzyme and a second end that is compatible with the second enzyme, under conditions favorable to ligation of compatible ends; and
- (f) selecting polynucleotides comprising a DNA fragment ligated to a vector molecule.
- 124. (previously presented): The method of claim 123, wherein the cell is selected from the group consisting of animal cells, plant cells and microbial cells.
- 125. (previously presented): The method of claim 123, wherein the first enzyme is a nuclease.
- 126. (previously presented): The method of claim 125, wherein the nuclease is DNase I.
- 127. (previously presented): The method of claim 125, wherein the nuclease is a restriction enzyme.

- 128. (previously presented): The method of claim 123, wherein the second enzyme is a restriction enzyme.
- 129. (previously presented): The method of claim 128, wherein the restriction enzyme is Sau3A I.
- 130. (previously presented): The method of claim 129, wherein the second end of the vector molecule is generated by digestion with BamH I.
- 131. (previously presented): The method of claim 126, wherein, subsequent to step (b), the DNase I ends are converted to blunt ends.
- 132. (previously presented): The method of claim 131, wherein the first end of the vector molecule is a blunt end.
- 133. (previously presented): The method of claim 132, wherein the first end of the vector molecule is generated by digestion with EcoRV or Smal.
- 134. (previously presented): The method of claim 123 wherein, during steps (b) (d), the nucleus is embedded in agarose.
- 135. (previously presented): The method of claim 123, wherein a plurality of different libraries of regulatory DNA sequences are prepared, wherein each library is obtained from a different cell.
- 136. (previously presented): The method of claim 135 wherein, in step (a), nuclei are obtained from cells at different stages of development.
- 137. (previously presented): The method of claim 135 wherein, in step (a), nuclei are obtained from cells in different tissues.
- 138. (previously presented): The method of claim 135 wherein, in step (a), nuclei are obtained from diseased cells and counterpart normal cells.

- 139. (previously presented): The method of claim 135 wherein, in step (a), nuclei are obtained from infected cells and counterpart uninfected cells.
- 140. (previously presented): The method of claim 135 wherein, in step (a), nuclei are obtained from cells that express a gene of interest at different levels.
- 141. (previously presented): The method of claim 123, wherein a plurality of different libraries of regulatory DNA sequences are prepared and, for each library, a different first enzyme is used.
- 142. (previously presented): The method of claim 141, wherein the different libraries are combined.
- 143. (currently amended): A method for isolating a collection of polynucleotides comprising cellular regulatory sequences, wherein the method comprises:
- (a) contacting cellular chromatin with a probe, wherein the probe reacts with accessible regions of cellular chromatin;
- (b) subsequently fragmenting the cellular chromatin to generate a eollection plurality of different polynucleotide fragments; and
- (c) selectively cloning polynucleotide fragments of step (b) comprising a site of probe reaction.
- 144. (previously presented): The method of claim 143, wherein reaction of the probe with cellular chromatin results in polynucleotide cleavage at the site of reaction.
- 145. (previously presented): The method of claim 143, wherein the cellular chromatin in present in an isolated nucleus.
- 146. (previously presented): The method of claim 145 wherein, in steps (a) and (b), the isolated nucleus is embedded in agarose.
- 147. (previously presented): The method of claim 143, wherein the probe is an enzyme.

PATENT USSN 09/844,501 Docket No. 8325-0015 Ref. No. S15-US1

- 148. (previously presented): The method of claim 147, wherein the enzyme is a nuclease.
- 149. (previously presented): The method of claim 148, wherein the nuclease is a restriction enzyme.
- 150. (previously presented): The method of claim 148, wherein the nuclease is DNase I.
- 151. (previously presented): The method of claim 143 wherein, in step (b), cellular chromatin is fragmented by restriction enzyme digestion.
- 152. (previously presented): The method of claim 151, wherein the restriction enzyme is Sau3A1.